

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/563,194  
Source: IFWP  
Date Processed by STIC: 1/13/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/563,194

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4      Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length     Sequence(s)          contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)          missing. If intentional, please insert the following lines for **each** skipped sequence:  
                               (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                               (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               This sequence is intentionally skipped  
  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)          missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                               <210> sequence id number  
                               <400> sequence id number  
                               000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                               Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                               In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10    Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>     Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                               Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                               (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa     "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

Show <1107 only  
once.

delete  
extra <1107's.

## RAW SEQUENCE LISTING

DATE: 01/13/2006

PATENT APPLICATION: US/10/563,194

TIME: 10:18:21

Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt

Output Set: N:\CRF4\01132006\J563194.raw

3 <110> APPLICANT: JENSEN, Jens Stougaard  
W--> 4 <110> APPLICANT: MADSEN, Lene Heegaard  
W--> 5 <110> APPLICANT: RADUTOIU, Elena Simona  
W--> 6 <110> APPLICANT: MADSEN, Esben Bjorn  
W--> 7 <110> APPLICANT: SANDAL, Niels Norgaard  
9 <120> TITLE OF INVENTION: Nod-factor perception  
11 <130> FILE REFERENCE: 09663.0066USWO  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/563,194  
14 <141> CURRENT FILING DATE: 2006-01-03  
16 <150> PRIOR APPLICATION NUMBER: PCT/DK2004/000478  
17 <151> PRIOR FILING DATE: 2004-07-02  
19 <150> PRIOR APPLICATION NUMBER: PA 2003 01010 DK  
20 <151> PRIOR FILING DATE: 2003-07-03  
22 <160> NUMBER OF SEQ ID NOS: 54  
24 <170> SOFTWARE: PatentIn version 3.2  
26 <210> SEQ ID NO: 1  
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28 <212> TYPE: DNA  
29 <213> ORGANISM: Lotus japonicus  
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36 <211> LENGTH: 29  
37 <212> TYPE: DNA  
38 <213> ORGANISM: Lotus japonicus  
40 <400> SEQUENCE: 2  
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46 <212> TYPE: DNA  
47 <213> ORGANISM: Lotus japonicus  
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53 <210> SEQ ID NO: 4  
54 <211> LENGTH: 39  
55 <212> TYPE: DNA  
56 <213> ORGANISM: synthetic sequence  
59 <220> FEATURE:  
60 <221> NAME/KEY: misc\_feature  
61 <222> LOCATION: (1)..(39)  
62 <223> OTHER INFORMATION: Oligo dT primer  
64 <400> SEQUENCE: 4  
65 gaccacgcgt atcgatgtcg actttttttt tttttttt 39

Does Not Comply  
Corrected Diskette Needed

pg 1, 6-7

invalid <213> response. See item 10 on  
Err Summary  
Sheet.

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Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt

Output Set: N:\CRF4\01132006\J563194.raw

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87 ttgttcccca cttcacaaac atggctgtct tctttcttac ctctggctct ctgagtcctt      180
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91 cagacttttc atgccctgtt gactcacctc cttcttgatg aacatatgtg acatacacag      300
93 ctgagtcctc aaatcttctg agcctgacaa acatatctga tatatttgat atcagtcctt      360
95 tgtccattgc aagagccagt aacatagatg cagggaagga caagctgggt ccaggccaag      420
97 tcttactggg acctgtaact tgcggttgcg ccggaacca ctcttctgcc aatacctcct      480
99 accaaatcca gctagggtgat agctacgact ttgttgcaac cactttatat gagaacctta      540
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153 caaattcagg caagttagtt aattgcattt gaaatacata tttctgctca gagatgggtga      2160
155 acatccatgc tccgaagctc atattaagtg tggtagctat tttcttttca tctttttggg      2220
157 gtgaatgcgt gttcatgtaa ctcgtaagg gttatatatt acagaagtcg tatacgtcgt      2280

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Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt

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164 <212> TYPE: DNA
165 <213> ORGANISM: Lotus japonicus GIFU
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172 ccagttggtg tgtggagagc tattttgtta tgctgacatc tgcaatttgc agggcatcta 180
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180 gagcttaagt ggcaaggcaa acgacattac tatacgaatt ggctttgtac cagaaacagg 420
182 gaacaaataa tattttacaa ataagctatt atcatgtcag ctcatttgtt caactttgat 480
184 ttgattaaaa attaaatgaa gttgaatttg ttgagctgct ttattatata tgccactgga 540
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190 acagtagcat ttagataatg aatgatcttg gttctcgcta agcatcaaac caatctctac 720
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242 acgtgtatga aatcgacgag ataatggaag ctacgaagga tttcagcgat gagtgaagg 2280
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248 tgaaaactaat ggggtgtctcc tcaggctatg atggaaaactg tttcttggtt tatgaatatg 2460
250 ctgaaaatgg gtctcttgct gagtggctgt tctcaaagtc ttcaggaacc ccaaactccc 2520
252 ttacatggtc tcaaaggata agcatagcag tggatgttgc tgtgggtctg caatacatgc 2580

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Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt

Output Set: N:\CRF4\01132006\J563194.raw

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256 actcgaactt caaggccaag atagcgaatt tcgcatggc cagaacttcg accaacccca 2700
258 tgatgcaaaa aatcgatgtc ttcgctttcg ggggtgcttct gatagagttg ctcaccggaa 2760
260 ggaaagccat gacaaccaag gagaacggcg aggtggttat gctgtggaag gatatgtggg 2820
262 agatctttga catagaagag aatagagagg agaggatcag aaaatggatg gatcctaatt 2880
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282 taagggtgta tatattacag aagtcgtata cgctgttcca ataattgatc aagggtacctg 3480
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289 <212> TYPE: PRT
290 <213> ORGANISM: Lotus japonicus
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299 20 25 30
302 Gly Pro Asp Phe Ser Cys Pro Val Asp Ser Pro Pro Ser Cys Glu Thr
303 35 40 45
306 Tyr Val Thr Tyr Thr Ala Gln Ser Pro Asn Leu Leu Ser Leu Thr Asn
307 50 55 60
310 Ile Ser Asp Ile Phe Asp Ile Ser Pro Leu Ser Ile Ala Arg Ala Ser
311 65 70 75 80
314 Asn Ile Asp Ala Gly Lys Asp Lys Leu Val Pro Gly Gln Val Leu Leu
315 85 90 95
318 Val Pro Val Thr Cys Gly Cys Ala Gly Asn His Ser Ser Ala Asn Thr
319 100 105 110
322 Ser Tyr Gln Ile Gln Leu Gly Asp Ser Tyr Asp Phe Val Ala Thr Thr
323 115 120 125
326 Leu Tyr Glu Asn Leu Thr Asn Trp Asn Ile Val Gln Ala Ser Asn Pro
327 130 135 140
330 Gly Val Asn Pro Tyr Leu Leu Pro Glu Arg Val Lys Val Val Phe Pro
331 145 150 155 160
334 Leu Phe Cys Arg Cys Pro Ser Lys Asn Gln Leu Asn Lys Gly Ile Gln
335 165 170 175
338 Tyr Leu Ile Thr Tyr Val Trp Lys Pro Asn Asp Asn Val Ser Leu Val
339 180 185 190
342 Ser Ala Lys Phe Gly Ala Ser Pro Ala Asp Ile Leu Thr Glu Asn Arg
343 195 200 205
346 Tyr Gly Gln Asp Phe Thr Ala Ala Thr Asn Leu Pro Ile Leu Ile Pro
347 210 215 220

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Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt

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351 225                230                235                240
354 Ser Ser Ile His Leu Leu Val Ile Leu Gly Ile Thr Leu Gly Cys Thr
355                245                250                255
358 Leu Leu Thr Ala Val Leu Thr Gly Thr Leu Val Tyr Val Tyr Cys Arg
359                260                265                270
362 Arg Lys Lys Ala Leu Asn Arg Thr Ala Ser Ser Ala Glu Thr Ala Asp
363                275                280                285
366 Lys Leu Leu Ser Gly Val Ser Gly Tyr Val Ser Lys Pro Asn Val Tyr
367 290                295                300
370 Glu Ile Asp Glu Ile Met Glu Ala Thr Lys Asp Phe Ser Asp Glu Cys
371 305                310                315                320
374 Lys Val Gly Glu Ser Val Tyr Lys Ala Asn Ile Glu Gly Arg Val Val
375                325                330                335
378 Ala Val Lys Lys Ile Lys Glu Gly Gly Ala Asn Glu Glu Leu Lys Ile
379                340                345                350
382 Leu Gln Lys Val Asn His Gly Asn Leu Val Lys Leu Met Gly Val Ser
383                355                360                365
386 Ser Gly Tyr Asp Gly Asn Cys Phe Leu Val Tyr Glu Tyr Ala Glu Asn
387 370                375                380
390 Gly Ser Leu Ala Glu Trp Leu Phe Ser Lys Ser Ser Gly Thr Pro Asn
391 385                390                395                400
394 Ser Leu Thr Trp Ser Gln Arg Ile Ser Ile Ala Val Asp Val Ala Val
395                405                410                415
398 Gly Leu Gln Tyr Met His Glu His Thr Tyr Pro Arg Ile Ile His Arg
399                420                425                430
402 Asp Ile Thr Thr Ser Asn Ile Leu Leu Asp Ser Asn Phe Lys Ala Lys
403                435                440                445
406 Ile Ala Asn Phe Ala Met Ala Arg Thr Ser Thr Asn Pro Met Met Pro
407 450                455                460
410 Lys Ile Asp Val Phe Ala Phe Gly Val Leu Leu Ile Glu Leu Leu Thr
411 465                470                475                480
414 Gly Arg Lys Ala Met Thr Thr Lys Glu Asn Gly Glu Val Val Met Leu
415                485                490                495
418 Trp Lys Asp Met Trp Glu Ile Phe Asp Ile Glu Glu Asn Arg Glu Glu
419                500                505                510
422 Arg Ile Arg Lys Trp Met Asp Pro Asn Leu Glu Ser Phe Tyr His Ile
423                515                520                525
426 Asp Asn Ala Leu Ser Leu Ala Ser Leu Ala Val Asn Cys Thr Ala Asp
427 530                535                540
430 Lys Ser Leu Ser Arg Pro Ser Met Ala Glu Ile Val Leu Ser Leu Ser
431 545                550                555                560
434 Phe Leu Thr Gln Gln Ser Ser Asn Pro Thr Leu Glu Arg Ser Leu Thr
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442 Thr Ala Arg
443 595
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<213> Glycine max

<220>  
<221> misc feature  
<222> (1). (27) *do you mean (26)?*  
<223> NPR5 gene PCR primers

<400> 45  
ctaatacgac ataccaacaa ctgcag

26

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/563,194

DATE: 01/13/2006

TIME: 10:18:22

Input Set : A:\SEQUENCE LISTING.txt-9663.66USWO.txt

Output Set: N:\CRF4\01132006\J563194.raw

L:4 M:280 W: Numeric Identifier already exists, <110> found multiple times  
L:5 M:280 W: Numeric Identifier already exists, <110> found multiple times  
L:6 M:280 W: Numeric Identifier already exists, <110> found multiple times  
L:7 M:280 W: Numeric Identifier already exists, <110> found multiple times  
L:13 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:1502 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 23  
L:1697 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:1720 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 23